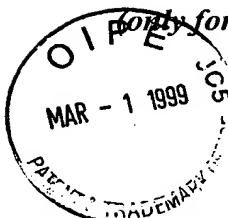


IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
CONTINUED PROSECUTION APPLICATION (CPA)
REQUEST TRANSMITTAL



Assistant Commissioner for Patents
Washington, D.C. 20231
BOX: CPA

Docket No.: 19603/468 (CRF D-1595C)
Express Mail No.: EL139239885US
Examiner: J.W. Ricigliano
Art Unit: 1648

16188
#19
K. Barman
3/24/99

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GROUP 180

This is a Request for filing a:

- ☒ continuation or
☐ divisional application

under 37 CFR 1.53(d), continued prosecution application, (CPA) of prior application number 08/794,851, filed on February 4, 1997, of Barany et al. entitled **DETECTION OF NUCLEIC ACID SEQUENCE DIFFERENCES USING THE LIGASE DETECTION REACTION WITH ADDRESSABLE ARRAYS.**

The above-identified prior pending application is hereby expressly abandoned as of the filing date of this request for a continued prosecution application (CPA).

1. ☐ Enter the unentered amendment previously filed on [*enter date] under 37 CFR 1.116 in the prior nonprovisional application.
2. ☒ A preliminary amendment is enclosed.
3. ☐ This application is filed by fewer than all the inventors named in the prior application, 37 CFR 1.53 (d)(4).
 - a. ☐ Delete the following inventor(s) named in the prior nonprovisional application:

03/04/1999 DVUONG 00000096 08794851

01 FC:131
02 FC:103

760.00 OP
1242.00 OP

- b. ☐ The inventor(s) to be deleted are set forth on a separate sheet enclosed herewith.
4. ☐ A new power of attorney is enclosed herewith.
5. ☐ Information Disclosure Statement (IDS) with PTO-1449 form(s) and copies of references are enclosed herewith.

03/24/1999 RHARMON 00000005 141138 08794851

01 FC:103 180.00 The filing fee is calculated on the basis of the claims existing in the prior application as

	(Col. 1)	(Col. 2)	SMALL ENTITY			LARGE ENTITY	
FOR:	NO. FILED	NO. EXTRA	RATE	FEE	OR	RATE	FEE
BASIC FEE	XXXXXXXXXX	XXXXXXXXXX	XXXXXX	\$380	OR	XXXXXX	\$760
TOTAL CLAIMS	89 - 20 =	69	x 9 =	\$	OR	x 18 =	\$1242
INDEP CLAIMS	1 - 3 =	0	x 39 =	\$	OR	x 78 =	\$
[] MULTIPLE DEPENDENT CLAIM PRESENTED			x130 =	\$	OR	x260 =	\$
*If the Total Claims are less than 20 and Indep. Claims are less than 3, enter "0" in Col. 2			TOTAL	\$	OR	TOTAL	\$2002

7. [X] A check in the amount of **\$2,002.00** is enclosed to cover the above filing fee.
8. [X] The Commissioner is hereby authorized to charge fees which may be required, or credit overpayment to Deposit Account No. 14-1138. A duplicate copy of this sheet is enclosed.
9. Small entity status:
 - [] A small entity statement is enclosed.
 - [] A small entity statement was filed in the prior nonprovisional application and such status is still proper and desired.
 - [] is no longer claimed.
10. [X] A copy of the Request for One-Month Extension of Time in prior application.
11. [X] A self-addressed, prepaid postcard for acknowledging receipt.
12. Other:

Address all future communications to (may only be completed by Applicant, or attorney or agent of record):

Michael L. Goldman
Nixon, Hargrave, Devans & Doyle LLP
Clinton Square
P.O. Box 1051
Rochester, New York 14603

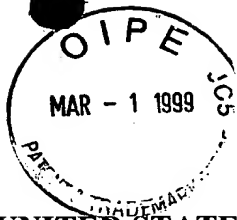
Respectfully submitted,



Michael L. Goldman
Registration No. 30,727

Date: March 1, 1999

Nixon, Hargrave, Devans & Doyle LLP
Clinton Square, P.O. Box 1051
Rochester, New York 14603
Telephone: (716) 263-1304
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Docket No.: 19603/468 (CRF D-1595C)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Barany et al.

Serial No. : CPA of 08/794,851

Filed : February 4, 1997

For : DETECTION OF NUCLEIC ACID
SEQUENCE DIFFERENCES USING THE
LIGASE DETECTION REACTION WITH
ADDRESSABLE ARRAYS

Examiner:
J.W. Ricigliano

Art Unit:
1648

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, D.C. 20231 -

Dear Sir:

Please cancel claims 89-137 without prejudice.

Please amend the above-identified patent application as follows:

In the Claims:

Please add new claim 148 as follows:

148. A method according to claim 1, wherein the capture oligonucleotides are in the form of DNA or PNA.

Please amend claims 1, 44, and 81 as follows:

1. (Amended) A method for identifying one or more of a plurality of sequences differing by one or more single-base changes, insertions, deletions, or translocations in a plurality of target nucleotide sequences comprising: